Human Genome Center

Leading genome research

he Human Genome Initiative is an international effort to locate and characterize the estimated 100,000 genes and sequence the three billion base pairs representing a human being. The Human Genome Center at Lawrence Livermore National Laboratory is a multidisciplinary effort, bringing together molecular biologists, chemists, physicists, mathematicians, computer scientists, and engineers to address these issues. The broad goals of our effort are to: 1) develop biological and physical resources useful for genome research; 2) couple these resources with novel strategies to

APPLICATIONS

- Physical map construction
- · DNA sequencing
- Disease (and other) gene identification
- Drug design
- · Gene therapy
- Studies in genome organization and variation

construct ordered clone maps and DNA sequences of human chromosomes; and 3) use the map and sequence information to study genome organization and variation.

The Center has focused its efforts on human chromosome 19, where it has generated a chromosome 19 metric physical map spanning ~92% of the chromosome. Working with over 200 collaborators, more

than 300 genes and genetic markers have been localized on cosmids and incorporated into the ordered map. Over 450 Kb of high accuracy genomic sequence has been completed, including three DNA repair genes.

Instrumentation and informatics support genomics research

Instrumentation and computations have been key to our success in both mapping and sequencing. We have developed automated devices for plaque picking, for DNA chemistries, for DNA isolation, and for preparation of high-density arrays of DNA on filters. We have integrated informatics support directly into our mapping and sequencing efforts. Software has been designed that integrates and displays cosmid, YAC, FISH, and restriction maps, as well as sequence, hybridization, and screening data. Our chromosome 19 genome data is available via the World Wide Web (URL: http://www-bio.llnl.gov/bbrp/genome/genome.html).

Availability: Clone resources for mapping and sequencing are essential to insure the success of this effort. Nonexclusive licensing agreements are currently being developed for library screening and clonal distribution of LLNL-constructed chromosome specific cosmid libraries for chromosomes 2, 3, 7, 9, 12, 18, 21, 22, X, and Y. We welcome discussions with potential partners and collaborators.

Contact

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